

**REMARKS**

Favorable reconsideration, reexamination, and allowance of the present patent application are respectfully requested in view of the foregoing amendments and the following remarks. The foregoing amendments do not add new matter and are fully supported by the originally filed claims, page 8, lines 20-24, page 15, lines 8-20, page 16, lines 13-23, page 17, lines 1-6, page 18, lines 10-15.

***Objection to the Specification***

At page 2 of the Office Action, the disclosure as a whole was objected to because it allegedly contains an embedded hyperlink and/or other form of browser-executable code. Applicant respectfully requests reconsideration of this objection.

The specification has been amended to remove portions of the embedded hyperlink in each instance, so that it is no longer browser-executable.

For at least the foregoing reasons, Applicant respectfully submits that the disclosure as a whole is not objectionable, and therefore respectfully requests withdrawal of the objection thereto.

***Rejection under 35 U.S.C. § 112, second paragraph***

In the Office Action, beginning at page 2, Claims 1-10 were rejected under 35 U.S.C. § 112, second paragraph, as reciting subject matters that allegedly are indefinite, more specifically in the recitation of “an ArcA protein does not normally function”, and “wherein the ArcA protein that normally functions is a protein”. Applicant respectfully requests reconsideration of this rejection.

The claims have been amended to recite “the production of ArcA protein is reduced or eliminated” and have further clarified the antecedent phrases. This amendment is based on the description at page 15, lines 16-18 of the specification. Applicants assert that the claims are definite and clear in its meaning and intent.

For at least the foregoing reasons, Applicant respectfully submits that Claims 1-10 fully comply with 35 U.S.C. § 112, second paragraph, and therefore respectfully requests withdrawal of the rejection thereof under 35 U.S.C. § 112.

In the Office Action, beginning at page 3, Claim 6 was further rejected under 35

U.S.C. § 112, second paragraph, as reciting subject matters that allegedly are indefinite. Applicant respectfully requests reconsideration of this rejection. Claim 6 was further rejected as being allegedly vague and indefinite in the recitation of “DNA hybridizable with the nucleotide sequence of nucleotide numbers 101 to 817 of SEQ ID NO: 31...”. Claim 6 has been amended by deletion of the allegedly indefinite phrases and insertion of the specific stringent conditions, and therefore, applicants assert this claim is definite and clear in its intent and meaning.

For at least the foregoing reasons, Applicant respectfully submits that Claims 1-10 fully comply with 35 U.S.C. § 112, second paragraph, and therefore respectfully requests withdrawal of the rejection thereof under 35 U.S.C. § 112.

***Rejection under 35 U.S.C. § 112, first paragraph***

In the Office Action, beginning at page 4, Claims 1-6 and 8-10 were rejected under 35 U.S.C. § 112, first paragraph, as reciting subject matters that allegedly fail to comply with the written description requirement. Applicant respectfully requests reconsideration of this rejection.

Attached as Exhibit A are alignments of ArcA protein *E. coli* with that of the other  $\gamma$ -proteobacteria. This data clearly demonstrates that the amino acid sequence of ArcA protein is highly conserved among  $\gamma$ -proteobacteria. As such, a person skilled in the art can obtain the homologous arcA gene from  $\gamma$ -proteobacterium other than *E. coli* and *Pantoea ananatis* based on the disclosed nucleotide sequence of arcA gene of *E. coli* (SEQ ID NO: 31) or *Pantoea ananatis* (SEQ ID NO:19), and use the obtained arcA gene to disrupt a chromosomal arcA gene in each  $\gamma$ -proteobacterium. Applicants assert the the description of SEQ ID NO:31 and SEQ ID NO:19 are sufficient to describe the genus of ArcA genes/proteins from other  $\gamma$ -proteobacterium, as one of skill in the art would be able to ascertain other species and their respective ArcA gene/protein sequences. Therefore, these two exemplified and described sequences constitute a representative number of species since the relevant structural properties are easily ascertained and determined due to the highly homologous nature of the ArcA genes/proteins among  $\gamma$ -proteobacterium.

Similarly, applicants assert that the description of *E. coli* and *Pantoea ananatis*

which have been modified so that an ArcA protein does not function normally are sufficient to adequately describe the genus of  $\gamma$ -proteobacterium encompassed by the claims. Specifically, as shown in the attached Exhibit A, the common feature of this genus of bacteria is their structural commonality of having a disrupted ArcA gene/protein. This common structural feature is present in any species of the genus, and is therefore sufficient to demonstrate possession of the genus of  $\gamma$ -proteobacterium.

For at least the foregoing reasons, Applicant respectfully submits that Claims 1-6 and 8-10 fully comply with 35 U.S.C. § 112, first paragraph, and therefore respectfully requests withdrawal of the rejection thereof under 35 U.S.C. § 112.

***Rejection under 35 U.S.C. § 102(b)***

In the Office Action, beginning at page 6, Claims 1-9 were rejected under 35 U.S.C. § 102(b), as reciting subject matters that allegedly are anticipated by Cotter et al. Applicant respectfully requests reconsideration of this rejection.

Claim 1 relates to a  $\gamma$ -proteobacterium including, *inter alia*, “a target substance synthesized via TCA cycle” and “as compared to a wild-type  $\gamma$ -proteobacterium”. Support for the subject matter in claim 1 can be found, e.g., at page 8, lines 23-24, and page 17, lines 4-6. Although Cotter et al. discloses arcA gene-disrupted strains, the strains described by Cotter et al. do not have an ability to produce a target substance synthesized via the tricarboxylic acid cycle in an amount more than an amount of the substance produced by a wild-type bacterium. In contrast, the strains used in the Examples of the present specification are strains modified to have an ability to produce a target substance synthesized via the tricarboxylic acid cycle. That is, the WC196 strain disclosed in Example 2 is an L-lysine-producing mutant strain as described in page 9, lines 23-24 of the specification, and the MG1655 $\Delta$  sucA strain in which sucA gene is disrupted is an L-glutamic acid-producing strain, as described in page 11, lines 5-9 of the specification.

For at least the foregoing reasons, Applicant respectfully submits that the subject matters of Claims 1-9 are not anticipated by Cotter et al., are therefore not unpatentable under 35 U.S.C. § 102(b), and therefore respectfully requests withdrawal of the rejection thereof under 35 U.S.C. § 102(b).

In the Office Action, beginning at page 7, Claims 1-10 were rejected under 35 U.S.C. § 102(b), as reciting subject matters that allegedly are anticipated by Iuchi et al. Applicant respectfully requests reconsideration of this rejection.

As stated above, the claims recite “a target substance synthesized via TCA cycle” and “as compared to a wild-type  $\gamma$ -proteobacterium”. Although Iuchi et al. discloses *arcA* gene-disrupted strains, the strains disclosed by Iuchi et al. do not have an ability to produce a target substance synthesized via TCA cycle in an amount more than an amount of the substance produced by a wild-type bacterium. In contrast, the strains used in the Examples of the present specification are strains modified to have an ability to produce a target substance synthesized via TCA cycle. That is, the WC196 strain disclosed in Example 2 is an L-lysine-producing mutant strain as described in page 9, lines 23-24 of the English specification, and the MG1655 $\Delta$  *sucA* strain in which *sucA* gene is disrupted is an L-glutamic acid-producing strain, as described in page 11, lines 5-9 of the English specification.

For at least the foregoing reasons, Applicant respectfully submits that the subject matters of Claims 1-10 are not anticipated by Iuchi et al., are therefore not unpatentable under 35 U.S.C. § 102(b), and therefore respectfully requests withdrawal of the rejection thereof under 35 U.S.C. § 102(b).

In the Office Action, beginning at page 6, Claims 1-10 were rejected under 35 U.S.C. § 102(b), as reciting subject matters that allegedly are anticipated by Nystrom et al. Applicant respectfully requests reconsideration of this rejection.

Similar to our arguments presented above, the claims recite “a target substance synthesized via TCA cycle” and “as compared to a wild-type  $\gamma$ -proteobacterium”. Although Nystrom et al. discloses *arcA* gene-disrupted strains, Nystrom et al. does not disclose strains which have an ability to produce a target substance synthesized via TCA cycle in an amount more than an amount of the substance produced by a wild-type bacterium. In contrast, the strains used in the Examples of the present specification are strains modified to have an ability to produce a target substance synthesized via TCA cycle. That is, the WC196 strain disclosed in Example 2 is an L-lysine-producing mutant

strain as described in page 9, lines 23-24 of the English specification, and the MG1655Δ sucA strain in which sucA gene is disrupted is an L-glutamic acid-producing strain, as described in page 11, lines 5-9 of the English specification.

For at least the foregoing reasons, Applicant respectfully submits that the subject matters of Claims 1-10 are not anticipated by Nystrom et al., are therefore not unpatentable under 35 U.S.C. § 102(b), and therefore respectfully requests withdrawal of the rejection thereof under 35 U.S.C. § 102(b).

In the Office Action, beginning at page 8, Claim 2 was rejected under 35 U.S.C. § 102(b), as reciting subject matters that allegedly are anticipated by Sugimoto et al.. Applicants note that the patent number listed on page 8 of the office action is incorrect. The correct patent number, which is listed correctly on the PTO-892, is 5,919,694. Applicant respectfully requests reconsideration of this rejection.

Claim 2 has been amended to limit the number of amino acid substitutions, deletions or insertions to “up to 10”. Therefore, this limitation clearly removes the disclosure of Sugimoto et al. as prior art.

For at least the foregoing reasons, Applicant respectfully submits that the subject matters of Claim 2 is not anticipated by Sugimoto et al., is therefore not unpatentable under 35 U.S.C. § 102(b), and therefore respectfully requests withdrawal of the rejection thereof under 35 U.S.C. § 102(b).

#### ***Rejection under 35 U.S.C. § 102(e)***

In the Office Action, beginning at page 9, Claims 1-10 were rejected under 35 U.S.C. § 102(e), as reciting subject matters that allegedly are anticipated by Cervin et al. Applicant respectfully requests reconsideration of this rejection.

Applicants hereby submit a translation of the priority documents and a verification by the translator, as Exhibit B. These documents are sufficient to effectively remove Cervin et al. as prior art since the priority date of July 12, 2002 can be relied upon by applicants, because the priority documents provide support for the claimed subject matter.

For at least the foregoing reasons, Applicant respectfully submits that the subject

matters of Claims 1-10 are not anticipated by Cervin et al., because Cervin et al. is not prior art to the claimed subject matter and therefore the claims are not unpatentable under 35 U.S.C. § 102(e), and therefore respectfully requests withdrawal of the rejection thereof under 35 U.S.C. § 102(e).

***Conclusion***

For at least the foregoing reasons, Applicant respectfully submits that the present patent application is in condition for allowance. An early indication of the allowability of the present patent application is therefore respectfully solicited.

If Examiner Vogel believes that a telephone conference with the undersigned would expedite passage of the present patent application to issue, she is invited to call on the number below.

It is not believed that extensions of time are required, beyond those that may otherwise be provided for in accompanying documents. However, if additional extensions of time are necessary to prevent abandonment of this application, then such extensions of time are hereby petitioned under 37 C.F.R. § 1.136(a), and the undersigned respectfully authorizes that our deposit account 50-3077 be charged any required fees.

Respectfully submitted,

By:   
Shelly Guest Cermak

Shelly Guest Cermak  
Registration No. 39,571

**U.S. P.T.O. Customer No. 38108**  
Cermak & Kenealy, LLP  
515 E. Braddock Road, Suite B  
Alexandria, VA 22314  
703.778.6608

Date: June 10, 2005

## EXHIBIT A

### ALIGNMENT DATA

In the alignment data, each accession number means the following species of  $\gamma$ -proteobacterium.

S4704	Shigella flexneri_2457T
SF4433	Shigella flexneri
C5488	E. coli_CFT073
ECs5359	E. coli_O157J
Z6004	E. coli_O157
JW4364	E. coli_J
B4401	E. coli
STM4598	Salmonella typhimurium
SC4443	Salmonella enterica subsp. enterica serovar Choleraesuis
T4637	Salmonella enterica subsp. enterica serovar Typhi Ty2
STY4947	Salmonella enterica subsp. enterica serovar Typhi
SPA4408	Salmonella enterica subsp. enterica serovar Paratyphi
YPTB0601	Yersinia pseudotuberculosis
YP3725	Yersinia pestis biovar Medievalis
Y3721	Yersinia pestis KIM
YP00458	Yersinia pestis
ECA3893	Erwinia carotovora
Plu0562	Photorhabdus luminescens
VC2368	Vibrio cholerae
VP0489	Vibrio parahaemolyticus
PBPRA0547	Photobacterium profundum
VF2120	Vibrio fischeri
VV0646	Vibrio vulnificus YJ016
VV10548	Vibrio vulnificus
PM0219	Pasteurella multocida
SO3988	Shewanella oneidensis
MS1504	Mannheimia succiniciproducens
HD0278	Haemophilus ducreyi
HI0884	Haemophilus influenzae
VF1570	Vibrio fischeri

BLASTP 2.2.10 [Oct-19-2004]

Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

Query= eco:b4401 arcA, dye, fexA, msp, seg, sfrA, cpxC; negative response regulator of genes in aerobic pathways, (sensors, ArcB and CpxA) (A)  
(238 letters)

Database: GENES+DGENES: GENES+DGENES (amino acid sequence)  
1,405,264 sequences; 537,705,622 total letters

Searching.....done

Sequences producing significant alignments:

Top 10	<input type="checkbox"/> Clear	Select operation	<input type="checkbox"/> Exec	Score	E
				(bits)	Value
<input checked="" type="checkbox"/> <u>sfx:S4704</u> arcA; negative response regulator of genes in aerobic ...				478	e-134
<input checked="" type="checkbox"/> <u>sfl:SF4433</u> arcA; negative response regulator of genes in aerobic...				478	e-134
<input checked="" type="checkbox"/> <u>ecc:c5488</u> arcA; aerobic respiration control protein arcA [KO:K02...				478	e-134
<input checked="" type="checkbox"/> <u>ecs:ECs5359</u> negative response regulator of genes in aerobic path...				478	e-134
<input checked="" type="checkbox"/> <u>ece:Z6004</u> arcA; negative response regulator of genes in aerobic ...				478	e-134
<input checked="" type="checkbox"/> <u>ecj:JW4364</u> arcA; Aerobic respiration control protein ArcA (Dye r...				478	e-134
<input checked="" type="checkbox"/> <u>eco:b4401</u> arcA, dye, fexA, msp, seg, sfrA, cpxC; negative respon...				478	e-134
<input checked="" type="checkbox"/> <u>stm:STM4598</u> arcA; response regulator (OmpR family) in two-compon...				477	e-134
<input checked="" type="checkbox"/> <u>sec:SC4443</u> arcA; response regulator (OmpR family) in two-compone...				477	e-134
<input checked="" type="checkbox"/> <u>stt:t4637</u> arcA; global response regulator [KO:K02483]				477	e-134
<input type="checkbox"/> <u>sty:STY4947</u> arcA; global response regulator [KO:K02483]				477	e-134
<input type="checkbox"/> <u>spt:SPA4408</u> arcA; global response regulator [KO:K02483]				474	e-133
<input type="checkbox"/> <u>yps:YPTB0601</u> arcA; response regulator (OmpR family), in two-comp...				445	e-124
<input type="checkbox"/> <u>ypm:YP3725</u> arcA; aerobic respiration control protein [KO:K02483]				445	e-124
<input type="checkbox"/> <u>ypk:y3721</u> arcA; negative response regulator of genes in aerobic ...				445	e-124
<input type="checkbox"/> <u>ype:YPO0458</u> arcA, dye, fexA, sfrA, seg, msp, cpxC; aerobic respi...				445	e-124
<input type="checkbox"/> <u>eca:ECA3893</u> arcA, cpxC, dye, fexA, msp, sfrA; aerobic respiratio...				445	e-124
<input type="checkbox"/> <u>plu:plu0562</u> arcA; negative response regulator of genes in aerobic...				442	e-123
<input type="checkbox"/> <u>vch:VC2368</u> fexA; aerobic respiration control protein FexA [KO:K0...				427	e-119
<input type="checkbox"/> <u>vpa:VP0489</u> fexA; aerobic respiration control protein FexA [KO:K0...				417	e-116
<input type="checkbox"/> <u>ppr:PBPR0547</u> fexA; putative aerobic respiration control protein...				412	e-114
<input type="checkbox"/> <u>vfi:VF2120</u> arcA; aerobic respiration control protein ArcA [KO:K0...				411	e-114
<input type="checkbox"/> <u>vvy:VV0646</u> fexA; aerobic respiration control protein FexA [KO:K0...				411	e-114
<input type="checkbox"/> <u>vvu:VV10548</u> fexA; aerobic respiration control protein FexA [KO:K...				411	e-114
<input type="checkbox"/> <u>pmu:PM0219</u> arcA; aerobic respiration control protein [KO:K02483]				394	e-108
<input type="checkbox"/> <u>son:S03988</u> arcA; aerobic respiration control protein ArcA [KO:K0...				392	e-108
<input type="checkbox"/> <u>msu:MS1504</u> ompR; response regulators consisting of a CheY-like r...				382	e-105
<input type="checkbox"/> <u>hdu:HD0278</u> arcA; aerobic respiration control protein ArcA [KO:K0...				377	e-103
<input type="checkbox"/> <u>hin:HI0884</u> arcA; aerobic respiration control protein arcA homolo...				374	e-103
<input type="checkbox"/> <u>vfi:VF1570</u> torR; TorCAD operon transcriptional regulatory protei...				217	2e-55

>sfx:S4704 arcA; negative response regulator of genes in aerobic pathways  
(sensors, ArcB and CpxA) [KO:K02483]  
Length = 238

Score = 478 bits (1230), Expect = e-134  
Identities = 238/238 (100%), Positives = 238/238 (100%)

Query: 1 MQTPHILIVEDELVTRNTLKS|FEAEGYDVFEATDGAEMHQILSEYDINLVIMDINLPGK 60  
MQTPHILIVEDELVTRNTLKS|FEAEGYDVFEATDGAEMHQILSEYDINLVIMDINLPGK  
Sbjct: 1 MQTPHILIVEDELVTRNTLKS|FEAEGYDVFEATDGAEMHQILSEYDINLVIMDINLPGK 60  
  
Query: 61 NGLLLARELREQANVALMFLTGRDNEVDKILGLE|GADDY|TKPFPRELTIRARNLLSR 120  
NGLLLARELREQANVALMFLTGRDNEVDKILGLE|GADDY|TKPFPRELTIRARNLLSR  
Sbjct: 61 NGLLLARELREQANVALMFLTGRDNEVDKILGLE|GADDY|TKPFPRELTIRARNLLSR 120  
  
Query: 121 TMNLGTVSEERRSVESYKFNGWELDINSRSL|GPDGEQYKLPSEFRAMLHFCENPGK1Q 180  
TMNLGTVSEERRSVESYKFNGWELDINSRSL|GPDGEQYKLPSEFRAMLHFCENPGK1Q  
Sbjct: 121 TMNLGTVSEERRSVESYKFNGWELDINSRSL|GPDGEQYKLPSEFRAMLHFCENPGK1Q 180  
  
Query: 181 SRAELKKMTGRELKPHDRTVDVTIRRIRKHFESTPDTPE||ATIHGEGYRFCGDLED 238  
SRAELKKMTGRELKPHDRTVDVTIRRIRKHFESTPDTPE||ATIHGEGYRFCGDLED  
Sbjct: 181 SRAELKKMTGRELKPHDRTVDVTIRRIRKHFESTPDTPE||ATIHGEGYRFCGDLED 238

>sfl:SF4433 arcA; negative response regulator of genes in aerobic pathways  
(sensors, ArcB and CpxA) [KO:K02483]  
Length = 238

Score = 478 bits (1230), Expect = e-134  
Identities = 238/238 (100%), Positives = 238/238 (100%)

Query: 1 MQTPHILIVEDELVTRNTLKS|FEAEGYDVFEATDGAEMHQILSEYDINLVIMDINLPGK 60  
MQTPHILIVEDELVTRNTLKS|FEAEGYDVFEATDGAEMHQILSEYDINLVIMDINLPGK  
Sbjct: 1 MQTPHILIVEDELVTRNTLKS|FEAEGYDVFEATDGAEMHQILSEYDINLVIMDINLPGK 60  
  
Query: 61 NGLLLARELREQANVALMFLTGRDNEVDKILGLE|GADDY|TKPFPRELTIRARNLLSR 120  
NGLLLARELREQANVALMFLTGRDNEVDKILGLE|GADDY|TKPFPRELTIRARNLLSR  
Sbjct: 61 NGLLLARELREQANVALMFLTGRDNEVDKILGLE|GADDY|TKPFPRELTIRARNLLSR 120  
  
Query: 121 TMNLGTVSEERRSVESYKFNGWELDINSRSL|GPDGEQYKLPSEFRAMLHFCENPGK1Q 180  
TMNLGTVSEERRSVESYKFNGWELDINSRSL|GPDGEQYKLPSEFRAMLHFCENPGK1Q  
Sbjct: 121 TMNLGTVSEERRSVESYKFNGWELDINSRSL|GPDGEQYKLPSEFRAMLHFCENPGK1Q 180  
  
Query: 181 SRAELKKMTGRELKPHDRTVDVTIRRIRKHFESTPDTPE||ATIHGEGYRFCGDLED 238  
SRAELKKMTGRELKPHDRTVDVTIRRIRKHFESTPDTPE||ATIHGEGYRFCGDLED  
Sbjct: 181 SRAELKKMTGRELKPHDRTVDVTIRRIRKHFESTPDTPE||ATIHGEGYRFCGDLED 238

>ecc:c5488 arcA; aerobic respiration control protein arcA [KO:K02483]  
Length = 238

Score = 478 bits (1230), Expect = e-134  
Identities = 238/238 (100%), Positives = 238/238 (100%)

Query: 1 MQTPHILIVEDELVTRNTLKS|FEAEGYDVFEATDGAEMHQILSEYDINLVIMDINLPGK 60  
MQTPHILIVEDELVTRNTLKS|FEAEGYDVFEATDGAEMHQILSEYDINLVIMDINLPGK  
Sbjct: 1 MQTPHILIVEDELVTRNTLKS|FEAEGYDVFEATDGAEMHQILSEYDINLVIMDINLPGK 60  
  
Query: 61 NGLLLARELREQANVALMFLTGRDNEVDKILGLE|GADDY|TKPFPRELTIRARNLLSR 120  
NGLLLARELREQANVALMFLTGRDNEVDKILGLE|GADDY|TKPFPRELTIRARNLLSR  
Sbjct: 61 NGLLLARELREQANVALMFLTGRDNEVDKILGLE|GADDY|TKPFPRELTIRARNLLSR 120

Query: 121 TMNLGTVSEERRSVESYKFNGWELDINSRSLIGPDGEQYKLPSEFRAMLHFCENPGKIQ 180  
TMNLGTVSEERRSVESYKFNGWELDINSRSLIGPDGEQYKLPSEFRAMLHFCENPGKIQ  
Sbjct: 121 TMNLGTVSEERRSVESYKFNGWELDINSRSLIGPDGEQYKLPSEFRAMLHFCENPGKIQ 180  
Query: 181 SRAELKKMTGRELKPHDRTVDTIRRIRKHFESTPDTPEIATIHGEGYRFCGLED 238  
SRAELKKMTGRELKPHDRTVDTIRRIRKHFESTPDTPEIATIHGEGYRFCGLED  
Sbjct: 181 SRAELKKMTGRELKPHDRTVDTIRRIRKHFESTPDTPEIATIHGEGYRFCGLED 238

>ecs:Ec5359 negative response regulator of genes in aerobic pathways ArcA  
[KO:K02483]  
Length = 238

Score = 478 bits (1230), Expect = e-134  
Identities = 238/238 (100%), Positives = 238/238 (100%)

Query: 1 MQTPHILIVEDELVTRNTLKSIFEAEGYDVFEATDGAEMHQILSEYDINLVIMDINLPGK 60  
MQTPHILIVEDELVTRNTLKSIFEAEGYDVFEATDGAEMHQILSEYDINLVIMDINLPGK  
Sbjct: 1 MQTPHILIVEDELVTRNTLKSIFEAEGYDVFEATDGAEMHQILSEYDINLVIMDINLPGK 60  
Query: 61 NGLLLARELREQANVALMFLTGRDNEVDKILGLEIGADDYITKPFNPRELTIRARNLLSR 120  
NGLLLARELREQANVALMFLTGRDNEVDKILGLEIGADDYITKPFNPRELTIRARNLLSR  
Sbjct: 61 NGLLLARELREQANVALMFLTGRDNEVDKILGLEIGADDYITKPFNPRELTIRARNLLSR 120  
Query: 121 TMNLGTVSEERRSVESYKFNGWELDINSRSLIGPDGEQYKLPSEFRAMLHFCENPGKIQ 180  
TMNLGTVSEERRSVESYKFNGWELDINSRSLIGPDGEQYKLPSEFRAMLHFCENPGKIQ  
Sbjct: 121 TMNLGTVSEERRSVESYKFNGWELDINSRSLIGPDGEQYKLPSEFRAMLHFCENPGKIQ 180  
Query: 181 SRAELKKMTGRELKPHDRTVDTIRRIRKHFESTPDTPEIATIHGEGYRFCGLED 238  
SRAELKKMTGRELKPHDRTVDTIRRIRKHFESTPDTPEIATIHGEGYRFCGLED  
Sbjct: 181 SRAELKKMTGRELKPHDRTVDTIRRIRKHFESTPDTPEIATIHGEGYRFCGLED 238

>ece:Z6004 arcA; negative response regulator of genes in aerobic pathways,  
(sensors, ArcB and CpxA) [KO:K02483]  
Length = 238

Score = 478 bits (1230), Expect = e-134  
Identities = 238/238 (100%), Positives = 238/238 (100%)

Query: 1 MQTPHILIVEDELVTRNTLKSIFEAEGYDVFEATDGAEMHQILSEYDINLVIMDINLPGK 60  
MQTPHILIVEDELVTRNTLKSIFEAEGYDVFEATDGAEMHQILSEYDINLVIMDINLPGK  
Sbjct: 1 MQTPHILIVEDELVTRNTLKSIFEAEGYDVFEATDGAEMHQILSEYDINLVIMDINLPGK 60  
Query: 61 NGLLLARELREQANVALMFLTGRDNEVDKILGLEIGADDYITKPFNPRELTIRARNLLSR 120  
NGLLLARELREQANVALMFLTGRDNEVDKILGLEIGADDYITKPFNPRELTIRARNLLSR  
Sbjct: 61 NGLLLARELREQANVALMFLTGRDNEVDKILGLEIGADDYITKPFNPRELTIRARNLLSR 120  
Query: 121 TMNLGTVSEERRSVESYKFNGWELDINSRSLIGPDGEQYKLPSEFRAMLHFCENPGKIQ 180  
TMNLGTVSEERRSVESYKFNGWELDINSRSLIGPDGEQYKLPSEFRAMLHFCENPGKIQ  
Sbjct: 121 TMNLGTVSEERRSVESYKFNGWELDINSRSLIGPDGEQYKLPSEFRAMLHFCENPGKIQ 180  
Query: 181 SRAELKKMTGRELKPHDRTVDTIRRIRKHFESTPDTPEIATIHGEGYRFCGLED 238  
SRAELKKMTGRELKPHDRTVDTIRRIRKHFESTPDTPEIATIHGEGYRFCGLED  
Sbjct: 181 SRAELKKMTGRELKPHDRTVDTIRRIRKHFESTPDTPEIATIHGEGYRFCGLED 238

>ecj:JW4364 arcA; Aerobic respiration control protein ArcA (Dye resistance  
protein) [KO:K02483]  
Length = 238

Score = 478 bits (1230), Expect = e-134  
Identities = 238/238 (100%), Positives = 238/238 (100%)

Query: 1 MQTPHILIVEDELVTRNTLKS1FEAEGYDVFEATDGAEMHQ1LSEYD1NLV1MD1NLPGK 60  
MQTPHILIVEDELVTRNTLKS1FEAEGYDVFEATDGAEMHQ1LSEYD1NLV1MD1NLPGK  
Sbjct: 1 MQTPHILIVEDELVTRNTLKS1FEAEGYDVFEATDGAEMHQ1LSEYD1NLV1MD1NLPGK 60  
  
Query: 61 NGLLLARELREQANVALMFLTGRDNEVDK1LGLE1GADDY1TKPFNPRELT1RARNLLSR 120  
NGLLLARELREQANVALMFLTGRDNEVDK1LGLE1GADDY1TKPFNPRELT1RARNLLSR  
Sbjct: 61 NGLLLARELREQANVALMFLTGRDNEVDK1LGLE1GADDY1TKPFNPRELT1RARNLLSR 120  
  
Query: 121 TMNLGTVSEERRSVESYKFNGWELD1NSRSL1GPDGEQYKLPSEFRAMLHFCENPGK1Q 180  
TMNLGTVSEERRSVESYKFNGWELD1NSRSL1GPDGEQYKLPSEFRAMLHFCENPGK1Q  
Sbjct: 121 TMNLGTVSEERRSVESYKFNGWELD1NSRSL1GPDGEQYKLPSEFRAMLHFCENPGK1Q 180  
  
Query: 181 SRAELKKMTGRELKPHDRTVDVT1RR1RKHFESTPDTPE11AT1HGEGYRFCGDLED 238  
SRAELKKMTGRELKPHDRTVDVT1RR1RKHFESTPDTPE11AT1HGEGYRFCGDLED  
Sbjct: 181 SRAELKKMTGRELKPHDRTVDVT1RR1RKHFESTPDTPE11AT1HGEGYRFCGDLED 238

>eco:b4401 arcA, dye, fexA, msp, seg, sfrA, cpxC; negative response regulator of genes in aerobic pathways, (sensors, ArcB and CpxA)  
[KO:K02483]  
Length = 238

Score = 478 bits (1230), Expect = e-134  
Identities = 238/238 (100%), Positives = 238/238 (100%)

Query: 1 MQTPHILIVEDELVTRNTLKS1FEAEGYDVFEATDGAEMHQ1LSEYD1NLV1MD1NLPGK 60  
MQTPHILIVEDELVTRNTLKS1FEAEGYDVFEATDGAEMHQ1LSEYD1NLV1MD1NLPGK  
Sbjct: 1 MQTPHILIVEDELVTRNTLKS1FEAEGYDVFEATDGAEMHQ1LSEYD1NLV1MD1NLPGK 60  
  
Query: 61 NGLLLARELREQANVALMFLTGRDNEVDK1LGLE1GADDY1TKPFNPRELT1RARNLLSR 120  
NGLLLARELREQANVALMFLTGRDNEVDK1LGLE1GADDY1TKPFNPRELT1RARNLLSR  
Sbjct: 61 NGLLLARELREQANVALMFLTGRDNEVDK1LGLE1GADDY1TKPFNPRELT1RARNLLSR 120  
  
Query: 121 TMNLGTVSEERRSVESYKFNGWELD1NSRSL1GPDGEQYKLPSEFRAMLHFCENPGK1Q 180  
TMNLGTVSEERRSVESYKFNGWELD1NSRSL1GPDGEQYKLPSEFRAMLHFCENPGK1Q  
Sbjct: 121 TMNLGTVSEERRSVESYKFNGWELD1NSRSL1GPDGEQYKLPSEFRAMLHFCENPGK1Q 180  
  
Query: 181 SRAELKKMTGRELKPHDRTVDVT1RR1RKHFESTPDTPE11AT1HGEGYRFCGDLED 238  
SRAELKKMTGRELKPHDRTVDVT1RR1RKHFESTPDTPE11AT1HGEGYRFCGDLED  
Sbjct: 181 SRAELKKMTGRELKPHDRTVDVT1RR1RKHFESTPDTPE11AT1HGEGYRFCGDLED 238

>stm:STM4598 arcA; response regulator (OmpR family) in two-component regulatory system with ArcB (or CpxA), regulates genes in aerobic pathways [KO:K02483]  
Length = 238

Score = 477 bits (1227), Expect = e-134  
Identities = 237/238 (99%), Positives = 238/238 (100%)

Query: 1 MQTPHILIVEDELVTRNTLKS1FEAEGYDVFEATDGAEMHQ1LSEYD1NLV1MD1NLPGK 60  
MQTPHILIVEDELVTRNTLKS1FEAEGYDVFEATDGAEMHQ1LSEYD1NLV1MD1NLPGK  
Sbjct: 1 MQTPHILIVEDELVTRNTLKS1FEAEGYDVFEATDGAEMHQ1LSEYD1NLV1MD1NLPGK 60  
  
Query: 61 NGLLLARELREQANVALMFLTGRDNEVDK1LGLE1GADDY1TKPFNPRELT1RARNLLSR 120  
NGLLLARELREQANVALMFLTGRDNEVDK1LGLE1GADDY1TKPFNPRELT1RARNLLSR  
Sbjct: 61 NGLLLARELREQANVALMFLTGRDNEVDK1LGLE1GADDY1TKPFNPRELT1RARNLLSR 120

Query: 121 TMNLGTVSEERRSVESYKFNGWELD|NSRSL|GPDGEQYKLPSEFRAMLHFCENPGK|Q 180  
TMNLGTVSEERRSVESYKFNGWELD|NSRSL|GPDGEQYKLPSEFRAMLHFCENPGK|Q  
Sbjct: 121 TMNLGTVSEERRSVESYKFNGWELD|NSRSL|GPDGEQYKLPSEFRAMLHFCENPGK|Q 180

Query: 181 SRAELKKMTGRELKPHRTVDVTIRRIRKHFESTPDTPE||ATIHGEGYRFGDLED 238  
SRAELKKMTGRELKPHRTVDVTIRRIRKHFESTPDTPE||ATIHGEGYRFGDLD+D  
Sbjct: 181 SRAELKKMTGRELKPHRTVDVTIRRIRKHFESTPDTPE||ATIHGEGYRFGDLDQD 238

>sec:SC4443 arcA; response regulator (OmpR family) in two-component regulatory system with ArcB (or CpxA), regulates genes in aerobic pathways  
Length = 238

Score = 477 bits (1227), Expect = e-134  
Identities = 237/238 (99%), Positives = 238/238 (100%)

Query: 1 MQTPHILIVEDELVTRNTLKS|FEAEGYDVFEATDGAEMHQILSEYDINLVIMDINLPGK 60  
MQTPHILIVEDELVTRNTLKS|FEAEGYDVFEATDGAEMHQILSEYDINLVIMDINLPGK  
Sbjct: 1 MQTPHILIVEDELVTRNTLKS|FEAEGYDVFEATDGAEMHQILSEYDINLVIMDINLPGK 60

Query: 61 NGLLLARELREQANVALMFLTGRDNEVDKILGLE|GADDY|TKPFNPRELT|RARNLLSR 120  
NGLLLARELREQANVALMFLTGRDNEVDKILGLE|GADDY|TKPFNPRELT|RARNLLSR  
Sbjct: 61 NGLLLARELREQANVALMFLTGRDNEVDKILGLE|GADDY|TKPFNPRELT|RARNLLSR 120

Query: 121 TMNLGTVSEERRSVESYKFNGWELD|NSRSL|GPDGEQYKLPSEFRAMLHFCENPGK|Q 180  
TMNLGTVSEERRSVESYKFNGWELD|NSRSL|GPDGEQYKLPSEFRAMLHFCENPGK|Q  
Sbjct: 121 TMNLGTVSEERRSVESYKFNGWELD|NSRSL|GPDGEQYKLPSEFRAMLHFCENPGK|Q 180

Query: 181 SRAELKKMTGRELKPHRTVDVTIRRIRKHFESTPDTPE||ATIHGEGYRFGDLED 238  
SRAELKKMTGRELKPHRTVDVTIRRIRKHFESTPDTPE||ATIHGEGYRFGDLD+D  
Sbjct: 181 SRAELKKMTGRELKPHRTVDVTIRRIRKHFESTPDTPE||ATIHGEGYRFGDLDQD 238

>stt:t4637 arcA; global response regulator [KO:K02483]  
Length = 238

Score = 477 bits (1227), Expect = e-134  
Identities = 237/238 (99%), Positives = 238/238 (100%)

Query: 1 MQTPHILIVEDELVTRNTLKS|FEAEGYDVFEATDGAEMHQILSEYDINLVIMDINLPGK 60  
MQTPHILIVEDELVTRNTLKS|FEAEGYDVFEATDGAEMHQILSEYDINLVIMDINLPGK  
Sbjct: 1 MQTPHILIVEDELVTRNTLKS|FEAEGYDVFEATDGAEMHQILSEYDINLVIMDINLPGK 60

Query: 61 NGLLLARELREQANVALMFLTGRDNEVDKILGLE|GADDY|TKPFNPRELT|RARNLLSR 120  
NGLLLARELREQANVALMFLTGRDNEVDKILGLE|GADDY|TKPFNPRELT|RARNLLSR  
Sbjct: 61 NGLLLARELREQANVALMFLTGRDNEVDKILGLE|GADDY|TKPFNPRELT|RARNLLSR 120

Query: 121 TMNLGTVSEERRSVESYKFNGWELD|NSRSL|GPDGEQYKLPSEFRAMLHFCENPGK|Q 180  
TMNLGTVSEERRSVESYKFNGWELD|NSRSL|GPDGEQYKLPSEFRAMLHFCENPGK|Q  
Sbjct: 121 TMNLGTVSEERRSVESYKFNGWELD|NSRSL|GPDGEQYKLPSEFRAMLHFCENPGK|Q 180

Query: 181 SRAELKKMTGRELKPHRTVDVTIRRIRKHFESTPDTPE||ATIHGEGYRFGDLED 238  
SRAELKKMTGRELKPHRTVDVTIRRIRKHFESTPDTPE||ATIHGEGYRFGDLD+D  
Sbjct: 181 SRAELKKMTGRELKPHRTVDVTIRRIRKHFESTPDTPE||ATIHGEGYRFGDLDQD 238

>sty:STY4947 arcA; global response regulator [KO:K02483]  
Length = 238

Score = 477 bits (1227), Expect = e-134

Identities = 237/238 (99%), Positives = 238/238 (100%)

Query: 1 MQTPHILIVEDELVTRNTLKS|FEAEGYDVFEATDGAEMHQILSEYDINLVIMDINLPGK 60  
MQTPHILIVEDELVTRNTLKS|FEAEGYDVFEATDGAEMHQILSEYDINLVIMDINLPGK  
Sbjct: 1 MQTPHILIVEDELVTRNTLKS|FEAEGYDVFEATDGAEMHQILSEYDINLVIMDINLPGK 60  
  
Query: 61 NGLLLARELREQANVALMFLTGRDNEVDKILGLE|GADDYITKPFNPRELTIRARNLLSR 120  
NGLLLARELREQANVALMFLTGRDNEVDKILGLE|GADDYITKPFNPRELTIRARNLLSR  
Sbjct: 61 NGLLLARELREQANVALMFLTGRDNEVDKILGLE|GADDYITKPFNPRELTIRARNLLSR 120  
  
Query: 121 TMNLGTVSEERRSVESYKFNGWELDINSRSL|GPDGEQYKLPSEFRAMLHFCENPGKIQ 180  
TMNLGTVSEERRSVESYKFNGWELDINSRSL|GPDGEQYKLPSEFRAMLHFCENPGKIQ  
Sbjct: 121 TMNLGTVSEERRSVESYKFNGWELDINSRSL|GPDGEQYKLPSEFRAMLHFCENPGKIQ 180  
  
Query: 181 SRAELKKMTGRELKPHDRTVDVTIRRIKHFESTPDTPEIIATIHGEGYRFCGDL 238  
SRAELKKMTGRELKPHDRTVDVTIRRIKHFESTPDTPEIIATIHGEGYRFCGDL+D  
Sbjct: 181 SRAELKKMTGRELKPHDRTVDVTIRRIKHFESTPDTPEIIATIHGEGYRFCGDLQD 238

>spt:SPA4408 arcA; global response regulator [KO:K02483]

Length = 238

Score = 474 bits (1219), Expect = e-133

Identities = 236/238 (99%), Positives = 237/238 (99%)

Query: 1 MQTPHILIVEDELVTRNTLKS|FEAEGYDVFEATDGAEMHQILSEYDINLVIMDINLPGK 60  
MQTPHILIVEDELVTRNTLKS|FEAEGYDVFEATDGAEMHQILSEYDINLVIMDINLPGK  
Sbjct: 1 MQTPHILIVEDELVTRNTLKS|FEAEGYDVFEATDGAEMHQILSEYDINLVIMDINLPGK 60  
  
Query: 61 NGLLLARELREQANVALMFLTGRDNEVDKILGLE|GADDYITKPFNPRELTIRARNLLSR 120  
NGLLLARELREQANVALMFLTGRDNEVDKILGLE|GADDYITKPFNPRELTIRARNLLSR  
Sbjct: 61 NGLLLARELREQANVALMFLTGRDNEVDKILGLE|GADDYITKPFNPRELTIRARNLLSR 120  
  
Query: 121 TMNLGTVSEERRSVESYKFNGWELDINSRSL|GPDGEQYKLPSEFRAMLHFCENPGKIQ 180  
TMNLGTVSEERRSVESYKFNGWELDINSRSL|GPDGEQYKLPSEFRAMLHFCENPGKIQ  
Sbjct: 121 TMNLGTVSEERRSVESYKFNGWELDINSRSL|GPDGEQYKLPSEFRAMLHFCENSQKIQ 180  
  
Query: 181 SRAELKKMTGRELKPHDRTVDVTIRRIKHFESTPDTPEIIATIHGEGYRFCGDL 238  
SRAELKKMTGRELKPHDRTVDVTIRRIKHFESTPDTPEIIATIHGEGYRFCGDL+D  
Sbjct: 181 SRAELKKMTGRELKPHDRTVDVTIRRIKHFESTPDTPEIIATIHGEGYRFCGDLQD 238

>yps:YPTB0601 arcA; response regulator (OmpR family), in two-component regulatory system with ArcB (or CpxA), regulates genes in aerobic respiration [KO:K02483]

Length = 238

Score = 445 bits (1145), Expect = e-124

Identities = 221/238 (92%), Positives = 227/238 (95%)

Query: 1 MQTPHILIVEDELVTRNTLKS|FEAEGYDVFEATDGAEMHQILSEYDINLVIMDINLPGK 60  
MQTPHILIVEDE+VTRNTLKS|FEAEGYV+EA DGAEMH ILSE DINLVIMDINLPGK  
Sbjct: 1 MQTPHILIVEDE+VTRNTLKS|FEAEGYV+EA DGAEMH ILSE DINLVIMDINLPGK 60  
  
Query: 61 NGLLLARELREQANVALMFLTGRDNEVDKILGLE|GADDYITKPFNPRELTIRARNLLSR 120  
NGLLLARELREQA+VALMFLTGRDNEVDKILGLE|GADDYITKPFNPRELTIRARNLLSR  
Sbjct: 61 NGLLLARELREQASVALMFLTGRDNEVDKILGLE|GADDYITKPFNPRELTIRARNLLSR 120  
  
Query: 121 TMNLGTVSEERRSVESYKFNGWELDINSRSL|GPDGEQYKLPSEFRAMLHFCENPGKIQ 180  
TMNL+V EERR VESYKFNGWELDINSRSL+P GE YKLPRSEFRAMLHFCENPGKIQ  
Sbjct: 121 TMNLSSVGEERRLVESYKFNGWELDINSRSLVSPTEHYKLPSEFRAMLHFCENPGKIQ 180

Query: 181 SRAELKKMTGRELKPHDRTVDVTIRRIRKFESTPDTPEIIATIHGEGYRFCGDLED 238  
SR ELLKKMTGRELKPHDRTVDVTIRRIRKFESTPDTPEIIATIHGEGYRFCGDLE+  
Sbjct: 181 SRGELKKMTGRELKPHDRTVDVTIRRIRKFESTPDTPEIIATIHGEGYRFCGDLEE 238

>ypm:YP3725 arcA; aerobic respiration control protein [KO:K02483]  
Length = 238

Score = 445 bits (1145), Expect = e-124  
Identities = 221/238 (92%), Positives = 227/238 (95%)

Query: 1 MQTPHILIVEDELVTRNTLKSIFEAEGYDVFEATDGAEMHQILSEYDINLVIMDINLPGK 60  
MQTPHILIVEDE+VTRNTLKSIFEAEGY V+EA DGAEMH ILSE DINLVIMDINLPGK  
Sbjct: 1 MQTPHILIVEDEVTRNTLKSIFEAEGYVYYANDGAEMHHILSENDINLVIMDINLPGK 60  
Query: 61 NGLLLARELREQANVALMFLTGRDNEVDKILGLE|GADDY|TKPFNPRELT|RARNLLSR 120  
NGLLLARELREQA+VALMFLTGRDNEVDKILGLE|GADDY|TKPFNPRELT|RARNLLSR  
Sbjct: 61 NGLLLARELREQASVALMFLTGRDNEVDKILGLE|GADDY|TKPFNPRELT|RARNLLSR 120  
Query: 121 TMNLGTVSEERRSVESYKFNGWELDINSRSLIGPDGEQYKLPSEFRAMLHFCENPGK1Q 180  
TMNL +V EERR VESYKFNGWELDINSRSL+ P GE YKLPRSEFRAMLHFCENPGK1Q  
Sbjct: 121 TMNLSSVGEERRLVESYKFNGWELDINSRSLVSPTEHYKLPSEFRAMLHFCENPGK1Q 180  
Query: 181 SRAELKKMTGRELKPHDRTVDVTIRRIRKFESTPDTPEIIATIHGEGYRFCGDLED 238  
SR ELLKKMTGRELKPHDRTVDVTIRRIRKFESTPDTPEIIATIHGEGYRFCGDLE+  
Sbjct: 181 SRGELKKMTGRELKPHDRTVDVTIRRIRKFESTPDTPEIIATIHGEGYRFCGDLEE 238

>ypk:y3721 arcA; negative response regulator of genes in aerobic pathways, sensors, ArcB and CpxA [KO:K02483]  
Length = 238

Score = 445 bits (1145), Expect = e-124  
Identities = 221/238 (92%), Positives = 227/238 (95%)

Query: 1 MQTPHILIVEDELVTRNTLKSIFEAEGYDVFEATDGAEMHQILSEYDINLVIMDINLPGK 60  
MQTPHILIVEDE+VTRNTLKSIFEAEGY V+EA DGAEMH ILSE DINLVIMDINLPGK  
Sbjct: 1 MQTPHILIVEDEVTRNTLKSIFEAEGYVYYANDGAEMHHILSENDINLVIMDINLPGK 60  
Query: 61 NGLLLARELREQANVALMFLTGRDNEVDKILGLE|GADDY|TKPFNPRELT|RARNLLSR 120  
NGLLLARELREQA+VALMFLTGRDNEVDKILGLE|GADDY|TKPFNPRELT|RARNLLSR  
Sbjct: 61 NGLLLARELREQASVALMFLTGRDNEVDKILGLE|GADDY|TKPFNPRELT|RARNLLSR 120  
Query: 121 TMNLGTVSEERRSVESYKFNGWELDINSRSLIGPDGEQYKLPSEFRAMLHFCENPGK1Q 180  
TMNL +V EERR VESYKFNGWELDINSRSL+ P GE YKLPRSEFRAMLHFCENPGK1Q  
Sbjct: 121 TMNLSSVGEERRLVESYKFNGWELDINSRSLVSPTEHYKLPSEFRAMLHFCENPGK1Q 180  
Query: 181 SRAELKKMTGRELKPHDRTVDVTIRRIRKFESTPDTPEIIATIHGEGYRFCGDLED 238  
SR ELLKKMTGRELKPHDRTVDVTIRRIRKFESTPDTPEIIATIHGEGYRFCGDLE+  
Sbjct: 181 SRGELKKMTGRELKPHDRTVDVTIRRIRKFESTPDTPEIIATIHGEGYRFCGDLEE 238

>ype:YP00458 arcA, dye, fexA, sfrA, seg, msp, cpxC; aerobic respiration control protein [KO:K02483]  
Length = 238

Score = 445 bits (1145), Expect = e-124  
Identities = 221/238 (92%), Positives = 227/238 (95%)

Query: 1 MQTPHILIVEDELVTRNTLKSIFEAEGYDVFEATDGAEMHQILSEYDINLVIMDINLPGK 60  
MQTPHILIVEDE+VTRNTLKSIFEAEGY V+EA DGAEMH ILSE DINLVIMDINLPGK

Subjct: 1 MQTPHILIVEDEIVTRNTLKSIFEAEQYVVYEANDGAEMHHILSENDINLVIMDINLPGK 60  
Query: 61 NGLLLARELREQANVALMFLTGRDNEVDKILGLEIGADDYITKPFNPRELTIRARNLLSR 120  
NGLLLARELREQA+VALMFLTGRDNEVDKILGLEIGADDYITKPFNPRELTIRARNLLSR  
Subjct: 61 NGLLLARELREQASVALMFLTGRDNEVDKILGLEIGADDYITKPFNPRELTIRARNLLSR 120  
Query: 121 TMNLGTVSEERRSVESYKFNGWELDINSRSLIGPDGEQYKLPSEFRAMLHFCENPGKIQ 180  
TMNL +V EERR VESYKFNGWELDINSRSL+ P GE YKLPRSEFRAMLHFCENPGKIQ  
Subjct: 121 TMNLSSVGEERRLVESYKFNGWELDINSRSLVPTGEHYKLPSEFRAMLHFCENPGKIQ 180  
Query: 181 SRAELKKMTGRELKPHDRTVDVTIRRIRKHFESTPDTPEIATIHGEGYRFCGDLED 238  
SR ELLKKMTGRELKPHDRTVDVTIRRIRKHFESTPDTPEIATIHGEGYRFCGDLE+  
Subjct: 181 SRGELKKMTGRELKPHDRTVDVTIRRIRKHFESTPDTPEIATIHGEGYRFCGDLEE 238

>eca:ECA3893 arcA, cpxC, dye, fexA, msp, sfrA; aerobic respiration control protein [KO:K02483]  
Length = 238

Score = 445 bits (1144), Expect = e-124  
Identities = 224/238 (94%), Positives = 228/238 (95%)

Query: 1 MQTPHILIVEDELVTRNTLKSIFEAEQYDVFEATDGAEMHQILSEYDINLVIMDINLPGK 60  
MQTPHILIVEDELVTRNTLKSIFEAEQYV EATDGAEMHILSE DINLVIMDINLPGK  
Subjct: 1 MQTPHILIVEDELVTRNTLKSIFEAEQYVVHEATDGAEMHHILSENDINLVIMDINLPGK 60  
Query: 61 NGLLLARELREQANVALMFLTGRDNEVDKILGLEIGADDYITKPFNPRELTIRARNLLSR 120  
NGLLLARELREQA VALMFLTGRDNEVDKILGLEIGADDYITKPFNPRELTIRARNLLSR  
Subjct: 61 NGLLLARELREQATVALMFLTGRDNEVDKILGLEIGADDYITKPFNPRELTIRARNLLSR 120  
Query: 121 TMNLGTVSEERRSVESYKFNGWELDINSRSLIGPDGEQYKLPSEFRAMLHFCENPGKIQ 180  
TMNLG+ +EERR VESY+FNGWELDINSRSLI P GEQYKLPSEFRAMLHFCENPGKIQ  
Subjct: 121 TMNLGSGTEERRLVESYRFNGWELDINSRSLISPAGEQYKLPSEFRAMLHFCENPGKIQ 180  
Query: 181 SRAELKKMTGRELKPHDRTVDVTIRRIRKHFESTPDTPEIATIHGEGYRFCGDLED 238  
SRAELKKMTGRELKPHDRTVDVTIRRIRKHFESTPDTPEIATIHGEGYRFCGDLE+  
Subjct: 181 SRAELKKMTGRELKPHDRTVDVTIRRIRKHFESTADTPEIATIHGEGYRFCGDLEN 238

>plu:plu0562 arcA; negative response regulator of genes in aerobic pathways, (sensors, ArcB and CpxA) (dye resistance protein) [KO:K02483]  
Length = 238

Score = 442 bits (1138), Expect = e-123  
Identities = 221/237 (93%), Positives = 226/237 (95%)

Query: 1 MQTPHILIVEDELVTRNTLKSIFEAEQYDVFEATDGAEMHQILSEYDINLVIMDINLPGK 60  
MQTPHILIVEDE+VTRNTLKSIFEAEQYV+EATDGAEMHILS DINLVIMDINLPGK  
Subjct: 1 MQTPHILIVEDEIVTRNTLKSIFEAEQYIVYEATDGESEMHILSNNDINLVIMDINLPGK 60  
Query: 61 NGLLLARELREQANVALMFLTGRDNEVDKILGLEIGADDYITKPFNPRELTIRARNLLSR 120  
NGLLLARELREQANVALMFLTGRDNEVDKILGLEIGADDYITKPFNPRELTIRARNLLSR  
Subjct: 61 NGLLLARELREQANVALMFLTGRDNEVDKILGLEIGADDYITKPFNPRELTIRARNLLSR 120  
Query: 121 TMNLGTVSEERRSVESYKFNGWELDINSRSLIGPDGEQYKLPSEFRAMLHFCENPGKIQ 180  
TMNL VSEERR VESYKFNGWELDINSRSLI P GE YKLPRSEFRAMLHFCENPGKIQ  
Subjct: 121 TMNLNSVSEERRQVESYKFNGWELDINSRSLISPAGEPYKLPSEFRAMLHFCENPGKIQ 180  
Query: 181 SRAELKKMTGRELKPHDRTVDVTIRRIRKHFESTPDTPEIATIHGEGYRFCGDLE 237  
+RA+LLKKMTGRELKPHDRTVDVTIRRIRKHFESTPDTPEIATIHGEGYRFCGDLE  
Subjct: 181 TRADLKKMTGRELKPHDRTVDVTIRRIRKHFESTPDTMEIATIHGEGYRFCGDLE 237

>vch:VC2368 fexA; aerobic respiration control protein FexA [KO:K02483]  
Length = 238

Score = 427 bits (1098), Expect = e-119  
Identities = 210/238 (88%), Positives = 223/238 (93%)

Query: 1 MQTPHILIVEDELVTRNTLKS1FEAEGYDVFEATDGAEMHQ1ILSEYD1NLV1MD1NLPGK 60  
MQTP ILIVEDE VTRNTLKS1FEAEGY VFEA++G EMHQ+LS+ INLV1MD1NLPGK  
Sbjct: 1 MQTPQILIVEEQVTRNTLKS1FEAEGYAVFEASNGEEMHQVLSDYP1NLV1MD1NLPGK 60  
  
Query: 61 NGLLLARELREQANVALMFLTGRDNEVDK1LGLE1GADDY1TKPFPRELT1RARNLLSR 120  
NGLLLARELREQA+VALMFLTGRDNEVDK1LGLE1GADDY1TKPFPRELT1RARNLLSR  
Sbjct: 61 NGLLLARELREQADVALMFLTGRDNEVDK1LGLE1GADDY1TKPFPRELT1RARNLLSR 120  
  
Query: 121 TMNLGTVSEERRSVESYKFNGWELD1NSRSL1GPDGEQYKLPSEFRAMLHFCENPGK1Q 180  
+M+ GT EE+RSVE Y FNGWELD1NSRSL+ PDG+ YKLPRSEFRA+LHFCEPGK1Q  
Sbjct: 121 SMHAGTTQEEKRSVEKYVFNGWELD1NSRSLVSPDGDSYKLPSEFRALLHFCENPGK1Q 180  
  
Query: 181 SRAELLKKMTGRELKPHDRTVDVT1RR1RKHFESTPDTPE11AT1HGEGYRFGDLED 238  
+RA+LLKKMTGRELKPHDRTVDVT1RR1RKHFES TPE11AT1HGEGYRFGDLED  
Sbjct: 181 TRADLLKKMTGRELKPHDRTVDVT1RR1RKHFESVSGTPE11AT1HGEGYRFGDLED 238

>vpa:VP0489 fexA; aerobic respiration control protein FexA [KO:K02483]  
Length = 238

Score = 417 bits (1073), Expect = e-116  
Identities = 206/238 (86%), Positives = 219/238 (92%)

Query: 1 MQTPHILIVEDELVTRNTLKS1FEAEGYDVFEATDGAEMHQ1ILSEYD1NLV1MD1NLPGK 60  
MQTP ILIVEDE VTRNTLKS1FEAEGY VFEA+DG EMHQ+LS+ INLV1MD1NLPGK  
Sbjct: 1 MQTPQILIVEEQVTRNTLKS1FEAEGYAVFEASDGEEMHQVLSDNS1NLV1MD1NLPGK 60  
  
Query: 61 NGLLLARELREQANVALMFLTGRDNEVDK1LGLE1GADDY1TKPFPRELT1RARNLLSR 120  
NGLLLARELREQAN+VALMFLTGRDNEVDK1LGLE1GADDY1TKPFPRELT1RARNLLSR  
Sbjct: 61 NGLLLARELREQAN1ALMFLTGRDNEVDK1LGLE1GADDY1TKPFPRELT1RARNLLSR 120  
  
Query: 121 TMNLGTVSEERRSVESYKFNGWELD1NSRSL1GPDGEQYKLPSEFRAMLHFCENPGK1Q 180  
+M+ V EE+RSVE Y+FNGW LD1NSRSL+ P G+ YKLPRSEFRA+LHFCEPGK1Q  
Sbjct: 121 SMSTNAVQEEKRSVEKYEFNGWLD1NSRSLVSPAGDSYKLPSEFRALLHFCENPGK1Q 180  
  
Query: 181 SRAELLKKMTGRELKPHDRTVDVT1RR1RKHFESTPDTPE11AT1HGEGYRFGDLED 238  
+RA+LLKKMTG ELKPHDRTVDVT1RR1RKHFES TPE11AT1HGEGYRFGDLED  
Sbjct: 181 TRADLLKKMTGGELKPHDRTVDVT1RR1RKHFESVSGTPE11AT1HGEGYRFGDLED 238

>ppr:PPRA0547 fexA; putative aerobic respiration control protein FexA [KO:K02483]  
Length = 239

Score = 412 bits (1060), Expect = e-114  
Identities = 199/238 (83%), Positives = 220/238 (92%)

Query: 1 MQTPHILIVEDELVTRNTLKS1FEAEGYDVFEATDGAEMHQ1ILSEYD1NLV1MD1NLPGK 60  
MQTPHILIVEDE VTRNTLKS1FEAEGY VFEA DGAEMHQ+LSE+ ++LV1MD1NLPGK  
Sbjct: 1 MQTPHILIVEDEHVTNTLKS1FEAEGYTVFEANDGAEMHQMLSEHPVHLV1MD1NLPGK 60  
  
Query: 61 NGLLLARELREQANVALMFLTGRDNEVDK1LGLE1GADDY1TKPFPRELT1RARNLLSR 120  
NGLLLARELREQ ++ALMFLTGRDNEVDK1LGLE1GADDY1TKPFPRELT1RARNLL+R  
Sbjct: 61 NGLLLARELREQGDALMFLTGRDNEVDK1LGLE1GADDY1TKPFPRELT1RARNLLTR 120

Query: 121 TMNLGTVSEERRSVESYKFNGWELDINSRSLIGPDGEQYKLPSEFRAMLHFCENPGKIQ 180  
MN G +E+++ VE Y+FNGW L+INSRSL+ P G+Q+KLPSEFRA+LHFCENPGKIQ  
Sbjct: 121 AMNQGLPTEDKKLVERYFNGWSLEINSRSLVSPSGDQFKLPRSEFRALLHFCENPGKIQ 180  
Query: 181 SRAELKKMTGRELKPHDRTVDVTIRRIRKHFESTPDTPEIATIHGEGYRFCGDLED 238  
+R +LLKKMTGRELKPHDRTVDVTIRRIRKHFES DTPEI+ATIHGEGYRFCGDLE+  
Sbjct: 181 TRGDLLKKMTGRELKPHDRTVDVTIRRIRKHFESVADTPEIVATIHGEGYRFCGDLN 238

>yfi:VF2120 arcA; aerobic respiration control protein ArcA [KO:K02483]  
Length = 239

Score = 411 bits (1056), Expect = e-114  
Identities = 200/238 (84%), Positives = 220/238 (92%)

Query: 1 MQTPHILIVEDELVTRNTLKSIFEAEGYDVFEATDGAEMHQILSEYDINLVIMDINLPGK 60  
MQTP ILIVEDE VTRNTLKSIFEAEGY+VFEA+DG EMH++LSE +NLVIMDINLPGK  
Sbjct: 1 MQTPQILIVEDEHVTTRNTLKSIFEAEGYNVFEASDGEEMHKVLSEQQLNLVIMDINLPGK 60  
Query: 61 NGLLLARELREQANVALMFLTGRDNEVDKILGLEIGADDYITKPFNPRELTIRARNLLSR 120  
NGLLLARELRE+ ++ALMFLTGRDNEVDKILGLEIGADDYITKPFNPRELTIRARNLL+R  
Sbjct: 61 NGLLLARELREQGDALMFLTGRDNEVDKILGLEIGADDYITKPFNPRELTIRARNLLTR 120  
Query: 121 TMNLGTVSEERRSVESYKFNGWELDINSRSLIGPDGEQYKLPSEFRAMLHFCENPGKIQ 180  
+MN TV E+++ VE Y FNGW ++INSRSL+ P GE YKLPSEFRA+LHFCENPGKIQ  
Sbjct: 121 SMNQNTVVEDKKMVERYVFNGWVTEINSRSLVSPSGESYKLPSEFRALLHFCENPGKIQ 180  
Query: 181 SRAELKKMTGRELKPHDRTVDVTIRRIRKHFESTPDTPEIATIHGEGYRFCGDLED 238  
+RA+LLKKMTGRELKPHDRTVDVTIRRIRKHFES DTPEI+ATIHGEGYRFCGDLE+  
Sbjct: 181 TRADLLKKMTGRELKPHDRTVDVTIRRIRKHFESVDTPEIATIHGEGYRFCGDLEE 238

>yvy:VV0646 fexA; aerobic respiration control protein FexA [KO:K02483]  
Length = 238

Score = 411 bits (1056), Expect = e-114  
Identities = 205/237 (86%), Positives = 218/237 (91%)

Query: 1 MQTPHILIVEDELVTRNTLKSIFEAEGYDVFEATDGAEMHQILSEYDINLVIMDINLPGK 60  
MQTP ILIVEDE VTRNTLKSIFEAEGY VFEA++G EMH +LSE +NLVIMDINLPGK  
Sbjct: 1 MQTPQILIVEDEQVTRNTLKSIFEAEGYAVFEASNGDEMHHMLSENSINLVIMDINLPGK 60  
Query: 61 NGLLLARELREQANVALMFLTGRDNEVDKILGLEIGADDYITKPFNPRELTIRARNLLSR 120  
NGLLLARELREQA+VALMFLTGRDNEVDKILGLEIGADDYITKPFNPRELTIRARNLLSR  
Sbjct: 61 NGLLLARELREQADVALMFLTGRDNEVDKILGLEIGADDYITKPFNPRELTIRARNLLSR 120  
Query: 121 TMNLGTVSEERRSVESYKFNGWELDINSRSLIGPDGEQYKLPSEFRAMLHFCENPGKIQ 180  
+M+ + EE+RSVE Y+FNGW LDINSRSLI P G+ YKLPSEFRA+LHFCENPGKIQ  
Sbjct: 121 SMSSSVMPPEEKRSVEKYEFGWVLDINSRSLISPSSGDGYKLPSEFRALLHFCENPGKIQ 180  
Query: 181 SRAELKKMTGRELKPHDRTVDVTIRRIRKHFESTPDTPEIATIHGEGYRFCGDLE 237  
+RA+LLKKMTGRELKPHDRTVDVTIRRIRKHFES TPEI+ATIHGEGYRFCGDLE  
Sbjct: 181 TRADLLKKMTGRELKPHDRTVDVTIRRIRKHFESVSGTPEIATIHGEGYRFCGDLE 237

>yvu:VV10548 fexA; aerobic respiration control protein FexA [KO:K02483]  
Length = 238

Score = 411 bits (1056), Expect = e-114  
Identities = 205/237 (86%), Positives = 218/237 (91%)

Query: 1 MQTPHILIVEDELVTRNTLKS1FEAEGYDVFEATDGAEMHQ1LSEYD1NLVIMD1NLPGK 60  
MQTP ILIVEDE VTRNTLKS1FEAEGY VFEA++G EMH +LSE INLVIMD1NLPGK  
Sbjct: 1 MQTPQILIVEDEQVTRNTLKS1FEAEGYAVFEASNGDEMHHMLSENS1NLVIMD1NLPGK 60

Query: 61 NGLLLARELREQANVALMFLTGRDNEVDK1LGLE1GADDY1TKPFNPRELT1RARNLLSR 120  
NGLLLARELREQA+VALMFLTGRDNEVDK1LGLE1GADDY1TKPFNPRELT1RARNLLSR  
Sbjct: 61 NGLLLARELREQADVALMFLTGRDNEVDK1LGLE1GADDY1TKPFNPRELT1RARNLLSR 120

Query: 121 TMNLGTVSEERRSVESYKFNGWELD1NSRSL1GPDGEQYKLPSEFRAMLHFCENPGK1Q 180  
+M+ + EE+RSVE Y+FNGW LD1NSRSL1 P G+ YKLPRSEFRA+LHFCENPGK1Q  
Sbjct: 121 SMSSSVMPPEEKRSVEKYEFGNGWVL1NSRSL1SPSGDGYKLPSEFRALLHFCENPGK1Q 180

Query: 181 SRAELKKMTGRELKPHDRTVDVT1RR1RKHFESTPDTPE1IATIHGEGYRFCGDLE 237  
+RA+LLKKMTGRELKPHDRTVDVT1RR1RKHFES TPE1IATIHGEGYRFCGDLE  
Sbjct: 181 TRADLLKKMTGRELKPHDRTVDVT1RR1RKHFESVSGTPE1IATIHGEGYRFCGDLE 237

>pmu:PM0219 arcA: aerobic respiration control protein [KO:K02483]  
Length = 236

Score = 394 bits (1011), Expect = e-108  
Identities = 194/237 (81%), Positives = 210/237 (88%), Gaps = 1/237 (0%)

Query: 1 MQTPHILIVEDELVTRNTLKS1FEAEGYDVFEATDGAEMHQ1LSEYD1NLVIMD1NLPGK 60  
M TP ILIVEDE +TRNTLKS1FEAEGY+VFEA DGA+MH+ILS INLVIMD1NLPGK  
Sbjct: 1 MGTPQILIVEDEA1TRNTLKS1FEAEGYEVFEADGAQMHR1LSNKV1NLVIMD1NLPGK 60

Query: 61 NGLLLARELREQANVALMFLTGRDNEVDK1LGLE1GADDY1TKPFNPRELT1RARNLLSR 120  
NGL+LARELRE N ALMFLTGRDNEVDK1LGLE1GADDY1TKPFNPRELT1RARNLL R  
Sbjct: 61 NGMLMLARELRETTNTALMFLTGRDNEVDK1LGLE1GADDY1TKPFNPRELT1RARNLLQR 120

Query: 121 TMNLGTVSEERRSVESYKFNGWELD1NSRSL1GPDGEQYKLPSEFRAMLHFCENPGK1Q 180  
TM + + +E Y+FNGW LD+NSR+L1 P+GE+YKLPRSEFRAMLHFCENPGK1Q  
Sbjct: 121 TMQENS-KDSHHPIEQYRFNGWTLDNSRTL1NPEGEEYKLPSEFRAMLHFCENPGK1Q 179

Query: 181 SRAELKKMTGRELKPHDRTVDVT1RR1RKHFESTPDTPE1IATIHGEGYRFCGDLE 237  
+R ELLKKMTGRELK P DRTVDVT1RR1RKHFES P+TPE1IATIHGEGYRFCG+LE  
Sbjct: 180 TREELLLKKMTGRELKPHDRTVDVT1RR1RKHFEDHPETPE1IATIHGEGYRFCGELE 236

>son:S03988 arcA: aerobic respiration control protein ArcA [KO:K02483]  
Length = 238

Score = 392 bits (1006), Expect = e-108  
Identities = 194/238 (81%), Positives = 209/238 (87%)

Query: 1 MQTPHILIVEDELVTRNTLKS1FEAEGYDVFEATDGAEMHQ1LSEYD1NLVIMD1NLPGK 60  
MQ PHILIVEDE VTRNTL+S1FEAEGY V EA DGAEMH+ + E INLV+MD1NLPGK  
Sbjct: 1 MQNPHILIVEDEAVTRNTLRS1FEAEGYVVTAEANDGAEMHKAMQENK1NLVIMD1NLPGK 60

Query: 61 NGLLLARELREQANVALMFLTGRDNEVDK1LGLE1GADDY1TKPFNPRELT1RARNLLSR 120  
NGLLLARELRE N+ L+FLTGRDNEVDK1LGLE1GADDY1TKPFNPRELT1RARNLL+R  
Sbjct: 61 NGLLLARELREINN1GL1FLTGRDNEVDK1LGLE1GADDY1TKPFNPRELT1RARNLLTR 120

Query: 121 TMNLGTVSEERRSVESYKFNGWELD1NSRSL1GPDGEQYKLPSEFRAMLHFCENPGK1Q 180  
+ G EE+ SVE Y+FN W L+1NSRSL+ P GE YKLPRSEFRAMLHF ENPGK1  
Sbjct: 121 VNSAGNEVEEKSSVEYYRFNDWSLE1NSRSLVSPQGESYKLPSEFRAMLHFV1ENPGK1L 180

Query: 181 SRAELKKMTGRELKPHDRTVDVT1RR1RKHFESTPDTPE1IATIHGEGYRFCGDLED 238  
+RA+LL KMTGRELKPHDRTVDVT1RR1RKHFES PDTPE1IATIHGEGYRFCG+LED  
Sbjct: 181 TRADLLKKMTGRELKPHDRTVDVT1RR1RKHFESLPDTPE1IATIHGEGYRFCGNLED 238

>msu:MS1504 ompR; response regulators consisting of a CheY-like receiver domain and a HTH DNA-binding domain [KO:K02483].  
Length = 236

Score = 382 bits (982), Expect = e-105  
Identities = 190/240 (79%), Positives = 209/240 (87%), Gaps = 7/240 (2%)

Query: 1 MQTPHILIVEDELVTRNTLKS1FEAEGYDVFEATDGAEMHQ1LSEYD1NLV1MD1NLPGK 60  
M +P 1LIVEDE VTRNTLKS1FEAEGY+VFEATDG +MHQ1+ +INLV+MD1NLPGK  
Sbjct: 1 MLSPQ1LIVEDET VTRNTLKS1FEAEGYEVFEATDGNQMHQ11ETQE1NLV1MD1NLPGK 60  
  
Query: 61 NGLLLARELREQANVALMFLTGRDNEVDK1LGLE1GADDY1TKPFNPRELT1RARNLLSR 120  
NGL+LARELRE+ N ALMFLTGRDNEVDK1LGLE1GADDY1TKPFNPREL 1RARNLL R  
Sbjct: 61 NGMLLARELREKTNTALMFLTGRDNEVDK1LGLE1GADDY1TKPFNPRELA1RARNLLHR 120  
  
Query: 121 TMNLGTVSEERRS—VESYKFNGWELD1NSRSL1GPDGEQYKLPRSEFRAMLHFCENPG 177  
TM E+ S V++Y+FNGW LD1N R+L1 P+ +YKLPRSEFRAMLHFCENPG  
Sbjct: 121 TM—AENEKNSNTHVDAYRFNGWTL1DKRAL1DPESVEYKLPRSEFRAMLHFCENPG 176  
  
Query: 178 KIQSRAELLKKMTGRELKPHDRTVDVT1RR1RKHFESTPDTPE11AT1HGEGRFCGDLE 237  
KIQ+R +LLKKMTGRELKP DRTVDVT1RR1RKHF E PDTPE11AT1HGEGRFCG++E  
Sbjct: 177 KIQTREDLLKKMTGRELKPHDRTVDVT1RR1RKHFEDHPDTPE11AT1HGEGRFCGE1E 236

>hdu:HDO278 arcA; aerobic respiration control protein ArcA [KO:K02483]  
Length = 237

Score = 377 bits (968), Expect = e-103  
Identities = 188/237 (79%), Positives = 204/237 (86%)

Query: 1 MQTPHILIVEDELVTRNTLKS1FEAEGYDVFEATDGAEMHQ1LSEYD1NLV1MD1NLPGK 60  
MQ P 1LIVEDELVTRNTLKS1FEAEGY+VFEA+DG EM+ 1L++ 1NLV1MD1NLPGK  
Sbjct: 1 MQNPQ1LIVEDELVTRNTLKS1FEAEGYEVFEASDGMT1LAQQT1NLV1MD1NLPGK 60  
  
Query: 61 NGLLLARELREQANVALMFLTGRDNEVDK1LGLE1GADDY1TKPFNPRELT1RARNLLSR 120  
NGL+LARELRE +ALMFLTGRDNEVDK1LGLE+GADDY1TKPFNPREL1RARNLL R  
Sbjct: 61 NGMLLARELRENTKMAALMFLTGRDNEVDK1LGLEVGADDY1TKPFNPRELT1RARNLLHR 120  
  
Query: 121 TMNLGTVSEERRSVESYKFNGWELD1NSRSL1GPDGEQYKLPRSEFRAMLHFCENPGK1Q 180  
TM ESY+FNGW LD+NSRSL1 P+GE KLPRSEFRA+LHFCENPGK1Q  
Sbjct: 121 TMLEKDKVSHSEQQESYRFNGWTL1DVNSRSL1TPEGE1NLKPRSEFRALLHFCENPGK1Q 180  
  
Query: 181 SRAELLKKMTGRELKPHDRTVDVT1RR1RKHFESTPDTPE11AT1HGEGRFCGDLE 237  
+R +LL KMTGRELKPHDRTVDVT1RR1RKHF E +TPE11 T1HGEGRFCG +E  
Sbjct: 181 TREDLLKKMTGRELKPHDRTVDVT1RR1RKHFEDHLNTPE11VT1HGEGRFCGQ1E 237

>hin:H10884 arcA; aerobic respiration control protein arcA homolog [KO:K02483]  
Length = 236

Score = 374 bits (960), Expect = e-103  
Identities = 183/237 (77%), Positives = 206/237 (86%), Gaps = 1/237 (0%)

Query: 1 MQTPHILIVEDELVTRNTLKS1FEAEGYDVFEATDGAEMHQ1LSEYD1NLV1MD1NLPGK 60  
M TP 1L+VEDE+VTRNTLK 1FEAEGYDVFEA +G EMH 1L+ ++INLV+MD1NLPGK  
Sbjct: 1 MTTPK1LVEDE1VTRNTLKG1FEAEGYDVFEAENGVEMHH1LANHN1NLV1MD1NLPGK 60  
  
Query: 61 NGLLLARELREQANVALMFLTGRDNEVDK1LGLE1GADDY1TKPFNPRELT1RARNLLSR 120  
NGLLLARELRE+ ++ L+FLTGRDNEVDK1LGLE1GADDY+TKPFNPRELT1RARNLL R

Sbjct: 61 NGLLLARELREELSLPLIFLTGRDNEVDKILGLEIGADDYLTKPFNPRLTIRARNLLHR 120  
 Query: 121 TMNLGTVSEERRSVESYKFNGWELDINSRSLIGPDGEQYKLPSEFRAMLHFCENPGKIQ 180  
 M E E Y+FNGW+LD+NS SLI P+G+++KLPSEFRAMLHFCENPGK+Q  
 Sbjct: 121 AMP-HQEKENFGREFYRFNGWKLDDLNHSLITPEGQEFLPRSEFRAMLHFCENPGKIQ 179  
 Query: 181 SRAELKKMTGRELKPHDRTVDVTIRRIRKHFESTPDTEIIATIHGEGYRFGDLE 237  
 +R ELLKKMTGRELKPHDRTVDVTIRRIRKHFE P+TP II TIHGEGYRFGD+  
 Sbjct: 180 TREELKKMTGRELKPDRTVDVTIRRIRKHFEDHPNTPNIIMTIHGEGYRFGDIE 236

>vfi:VF1570 torR; TorCAD operon transcriptional regulatory protein TorR

[KO:KO2483]

Length = 232

Score = 217 bits (552), Expect = 2e-55  
 Identities = 110/231 (47%), Positives = 152/231 (65%), Gaps = 2/231 (0%)

Query: 5 HILIVEDELVTRNTLKSIFEAEQYDVFEATDGAEMHQILSEYDINLVIMDINLPGKNGLL 64  
 HIL+VEDE+VTR+ L FEAEGY V EA GAEM IL+E ++L+++DINLPG++GLL  
 Sbjct: 4 HILVVEDEVVTRSKLVGYFEAEQYQVSEAETGAEMRSILAEQKVDLIMLDINLPGEDGLL 63  
 Query: 65 LARELREQANVALMFLTGRDNEVDKILGLEIGADDYITKPFNPRLTIRARNLLSRTMNL 124  
 LARELR Q+N+ ++ +TGR + +D+I+GLE+GADDY+TKP REL +R +NL R M+L  
 Sbjct: 64 LARELRSQSNIGILVLTGRRTSDIDRIVGLEMGADDYVTKPVELRELLVRVKNLFWR-MSL 122  
 Query: 125 GTVSEERRSVESYKFNGWELDINSRSLIGPDGEQYKLPSEFRAMLHFCENPGKIQSRAE 184  
 E +F W DI R+L +GE KL ++E+ ++ P + SR  
 Sbjct: 123 ANEPVELDESNVVRGEWTFD1QRRAL-SNNGEPVKLTKAELYLLVALSSYPTVLSRER 181  
 Query: 185 LLKKMTGRELKPHDRTVDVTIRRIRKHFESTPDTEIIATIHGEGYRFGD 235  
 +L ++ R P+DRT+DV IRR+R E P P+I T+HGEGY F GD  
 Sbjct: 182 ILNMISHRVDAPNDRTIDVLIRRMRAKMEVDPKNPQIFVTVHGEQYMFAGD 232

Database: GENES+DGENES: GENES+DGENES(amino acid sequence)

Posted date: Jun 6, 2005 5:28 AM

Number of letters in database: 319,922,540

Number of sequences in database: 911,393

Database: dgenes

Posted date: Jun 4, 2005 8:12 AM

Number of letters in database: 217,783,082

Number of sequences in database: 493,871

Lambda	K	H
0.319	0.138	0.396

Gapped	Lambda	K	H
	0.267	0.0410	0.140

Matrix: BLOSUM62

Gap Penalties: Existence: 11, Extension: 1

Number of Hits to DB: 249,767,882

Number of Sequences: 1405264

Number of extensions: 9983109

Number of successful extensions: 34529

Number of sequences better than 10.0: 30

Number of HSP's better than 10.0 without gapping: 3346

Number of HSP's successfully gapped in prelim test: 1949

Number of HSP's that attempted gapping in prelim test: 26334

Number of HSP's gapped (non-prelim): 5566  
length of query: 238  
length of database: 537,705,622  
effective HSP length: 121  
effective length of query: 117  
effective length of database: 367,668,678  
effective search space: 43017235326  
effective search space used: 43017235326  
T: 11  
A: 40  
X1: 16 ( 7.4 bits)  
X2: 38 (14.6 bits)  
X3: 64 (24.7 bits)  
S1: 41 (21.7 bits)  
S2: 72 (32.3 bits)